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Application No: 10579290 Version No: 2.0

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<110> PATRYS PTY LIMITED

VOLLMER, Heinz

MULLER-HERMELINK, Hans-Konrad

<120> Human Monoclonal Antibody

<130> 043043-0359295

<140> 10579290

<141> 2010-07-12

<150> EP 03 026 161.4

<151> 2003-11-14

<160> 4

<170> PatentIn version 3.3

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<223> variable region of the light chain (VL) of antibody SAM-6

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Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Ser Pro Gly
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Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Asp Lys
20 25 30

Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu
35 40 45

Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg
50 55 60

Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser
65 70 75

Gly Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp
80 85 90

Asp Ser Ser Ile Val Val

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Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly

1 5 10 15

cag aca gcc agc atc acc tgc tct gga gat aaa ttg ggg gat aaa 90
Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Asp Lys

20 25 30

tat gct tgc tgg tat cag cag aag cca ggc cag tcc cct gtg ctg 135
Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu

35 40 45

gtc atc tat caa gat agc aag cgg ccc tca ggg atc cct gag cga 180
Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg

50 55 60

ttc tct ggc tcc aac tct ggg aac aca gcc act ctg acc atc agc 225
Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser

65 70 75

ggg acc cag gct atg gat gag gct gac tat tac tgt cag gcg tgg 270
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80 85 90

gac agc agc att gtg gta

288

Asp Ser Ser Ile Val Val

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<210> 3

<211> 110

<212> PRT

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<221> misc_feature

<223> variable region of the heavy chain (VH) of antibody SAM-6

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly
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Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr
50 55 60

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
65 70 75

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
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Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Leu Ala Val Ala Gly
95 100 105

Arg Pro Phe Asp Tyr
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Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly
1 5 10 15

agg tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt 90
Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
20 25 30

agc tat gct atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg 135
Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

gag tgg gtg gca gtt ata tca tat gat gga agc aat aaa tac tac 180
Glu Trp Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr
50 55 60

gca gac tcc gtg aag ggc cga ttc acc atc tcc aga gac aat tcc 225
Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
65 70 75

aag aac acg ctg tat ctg caa atg aac agc ctg aga gct gag gac 270
Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
80 85 90

acg gct gtg tat tac tgt gcg aga gat cgg tta gca gtg gct ggt 315
Thr Ala Val Tyr Tyr Cys Ala Arg Asp Arg Leu Ala Val Ala Gly
95 100 105

aga cct ttt gac tac 330
Arg Pro Phe Asp Tyr
110